



SEQUENCE LISTING

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SUZUKI, YOSHIHISA

<120> PYK2 CRYSTAL STRUCTURE AND USES

<130> 039363/1202

<140> 10/789,818
<141> 2004-02-27

<150> 60/451,101
<151> 2003-02-28

<160> 25

<170> PatentIn Ver. 3.2

<210> 1
<211> 272
<212> PRT
<213> Homo sapiens

<400> 1
Ile Ala Arg Glu Asp Val Val Leu Asn Arg Ile Leu Gly Glu Gly Phe
1 5 10 15
Phe Gly Glu Val Tyr Glu Gly Val Tyr Thr Asn His Lys Gly Glu Lys
20 25 30
Ile Asn Val Ala Val Lys Thr Cys Lys Lys Asp Cys Thr Leu Asp Asn
35 40 45
Lys Glu Lys Phe Met Ser Glu Ala Val Ile Met Lys Asn Leu Asp His
50 55 60
Pro His Ile Val Lys Leu Ile Gly Ile Ile Glu Glu Pro Thr Trp
65 70 75 80
Ile Ile Met Glu Leu Tyr Pro Tyr Gly Glu Leu Gly His Tyr Leu Glu
85 90 95
Arg Asn Lys Asn Ser Leu Lys Val Leu Thr Leu Val Leu Tyr Ser Leu
100 105 110
Gln Ile Cys Lys Ala Met Ala Tyr Leu Glu Ser Ile Asn Cys Val His
115 120 125
Arg Asp Ile Ala Val Arg Asn Ile Leu Val Ala Ser Pro Glu Cys Val
130 135 140
Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Ile Glu Asp Glu Asp Tyr
145 150 155 160

Tyr Lys Ala Ser Val Thr Arg Leu Pro Ile Lys Trp Met Ser Pro Glu
 165 170 175
 Ser Ile Asn Phe Arg Arg Phe Thr Thr Ala Ser Asp Val Trp Met Phe
 180 185 190
 Ala Val Cys Met Trp Glu Ile Leu Ser Phe Gly Lys Gln Pro Phe Phe
 195 200 205
 Trp Leu Glu Asn Lys Asp Val Ile Gly Val Leu Glu Lys Gly Asp Arg
 210 215 220
 Leu Pro Lys Pro Asp Leu Cys Pro Pro Val Leu Tyr Thr Leu Met Thr
 225 230 235 240
 Arg Cys Trp Asp Tyr Asp Pro Ser Asp Arg Pro Arg Phe Thr Glu Leu
 245 250 255
 Val Cys Ser Leu Ser Asp Val Tyr Gln Met Glu Lys Asp Ile Ala Met
 260 265 270

<210> 2
 <211> 293
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 pET15S protein containing PYK2

<400> 2
 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15
 Arg Gly Ser His Met Ile Ala Arg Glu Asp Val Val Leu Asn Arg Ile
 20 25 30
 Leu Gly Glu Gly Phe Phe Gly Glu Val Tyr Glu Gly Val Tyr Thr Asn
 35 40 45
 His Lys Gly Glu Lys Ile Asn Val Ala Val Lys Thr Cys Lys Lys Asp
 50 55 60
 Cys Thr Leu Asp Asn Lys Glu Lys Phe Met Ser Glu Ala Val Ile Met
 65 70 75 80
 Lys Asn Leu Asp His Pro His Ile Val Lys Leu Ile Gly Ile Ile Glu
 85 90 95
 Glu Glu Pro Thr Trp Ile Ile Met Glu Leu Tyr Pro Tyr Gly Glu Leu
 100 105 110
 Gly His Tyr Leu Glu Arg Asn Lys Asn Ser Leu Lys Val Leu Thr Leu
 115 120 125

Val Leu Tyr Ser Leu Gln Ile Cys Lys Ala Met Ala Tyr Leu Glu Ser
 130 135 140
 Ile Asn Cys Val His Arg Asp Ile Ala Val Arg Asn Ile Leu Val Ala
 145 150 155 160
 Ser Pro Glu Cys Val Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Ile
 165 170 175
 Glu Asp Glu Asp Tyr Tyr Lys Ala Ser Val Thr Arg Leu Pro Ile Lys
 180 185 190
 Trp Met Ser Pro Glu Ser Ile Asn Phe Arg Arg Phe Thr Thr Ala Ser
 195 200 205
 Asp Val Trp Met Phe Ala Val Cys Met Trp Glu Ile Leu Ser Phe Gly
 210 215 220
 Lys Gln Pro Phe Phe Trp Leu Glu Asn Lys Asp Val Ile Gly Val Leu
 225 230 235 240
 Glu Lys Gly Asp Arg Leu Pro Lys Pro Asp Leu Cys Pro Pro Val Leu
 245 250 255
 Tyr Thr Leu Met Thr Arg Cys Trp Asp Tyr Asp Pro Ser Asp Arg Pro
 260 265 270
 Arg Phe Thr Glu Leu Val Cys Ser Leu Ser Asp Val Tyr Gln Met Glu
 275 280 285
 Lys Asp Ile Ala Met
 290

<210> 3
 <211> 816
 <212> DNA
 <213> Homo sapiens

<400> 3
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 tatgaaggtg tctacacaaa tcacaaaggg gagaaaatca atgttagctgt caagacctgc 120
 aagaaaagact gcactctgga caacaaggag aagttcatga gcgaggcagt gatcatgaag 180
 aacctcgacc acccgacat cgtgaagctg atcggcatca ttgaagagga gcccacctgg 240
 atcatcatgg aattgtatcc ctaggggg ctggggccact acctggagcg gaacaagaac 300
 tccctgaagg tgctcacccct cgtgctgtac tcactgcaga tatgcaaagc catggcctac 360
 ctggagagca tcaactgcgt gcacagggac attgctgtcc ggaacatcct gttggcctcc 420
 cctgagtgtg tgaagctggg ggactttggt ctttcccggt acattgagga cgaggactat 480
 tacaaagcct ctgtgactcg tctcccccattc aaatggatgt ccccagagtc cattaacttc 540
 cgacgcttca cgacagccag tgacgtctgg atgttcgccc tgtgcattgtg ggagatcctg 600
 agcttggga agcagccctt cttctggctg gagaacaagg atgtcatcgg ggtgctggag 660
 aaaggagacc ggctgcccac gcctgatctc tgtccaccgg tccttatac cctcatgacc 720
 cgctgctggg actacgaccc cagtgaccgg ccccgcttca ccgagctggt gtgcagcctc 780
 agtgacgttt atcagatgga gaaggacatt gccatg 816

<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (108)..(170)

<220>
<223> Description of Artificial Sequence: Synthetic
pET15S multi-cloning site nucleotide sequence

<400> 7
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ttccccctcta gaaataattt tgtttaactt taagaaggag atatacc atg ggc agc 116
Met Gly Ser
1
agc cat cat cat cat cac agc agc ggc ctg gtg ccg cgc ggc agc 164
Ser His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
5 10 15
cat atg ggatccggaa ttcaaaggcc tacgtcgact agagcctgca gtctcgacca 220
His Met
20
tcatcatcat catcatataat aaaagggcga attccagcac actggcggcc gttacttagtg 280
gatccggctg ctaacaaagc ccgaaaggaa gctgagttgg ctgctgccac cgctgagcaa 340
taactagcat aacccttgg ggcctctaaa cgggtcttga ggggtttttt g 391

<210> 8
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
pET15S multi-cloning site peptide sequence

<400> 8
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15
Arg Gly Ser His Met
20

<210> 9
<211> 310
<212> PRT
<213> Unknown Organism

<220>

<223> Description of Unknown Organism: FAK tyrosine kinase
sequence

<400> 9

Glu Ile Gln Arg Glu Arg Ile Glu Leu Gly Arg Cys Ile Gly Glu Gly
1 5 10 15Gln Phe Gly Asp Val His Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro
20 25 30Ala Leu Ala Val Ala Ile Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser
35 40 45Val Arg Glu Lys Phe Leu Gln Glu Ala Cys His Tyr Thr Ser Leu His
50 55 60Trp Asn Trp Cys Arg Tyr Ile Ser Asp Pro Asn Val Asp Ala Cys Pro
65 70 75 80Asp Pro Arg Asn Ala Glu Leu Thr Met Arg Gln Phe Asp His Pro His
85 90 95Ile Val Lys Leu Ile Gly Val Ile Thr Glu Asn Pro Val Trp Ile Ile
100 105 110Met Glu Leu Cys Thr Leu Gly Glu Leu Arg Ser Phe Leu Gln Val Arg
115 120 125Lys Tyr Ser Leu Asp Leu Ala Ser Leu Ile Leu Tyr Ala Tyr Gln Leu
130 135 140Ser Thr Ala Leu Ala Tyr Leu Glu Ser Lys Arg Phe Val His Arg Asp
145 150 155 160Ile Ala Ala Arg Asn Val Leu Val Ser Ser Asn Asp Cys Val Lys Leu
165 170 175Gly Asp Phe Gly Leu Ser Arg Tyr Met Glu Asp Ser Thr Tyr Tyr Lys
180 185 190Ala Ser Lys Gly Lys Leu Pro Ile Lys Trp Met Ala Pro Glu Ser Ile
195 200 205Asn Phe Arg Arg Phe Thr Ser Ala Ser Asp Val Trp Met Phe Gly Val
210 215 220Cys Met Trp Glu Ile Leu Met His Gly Val Lys Pro Phe Gln Gly Val
225 230 235 240Lys Asn Asn Asp Val Ile Gly Arg Ile Glu Asn Gly Glu Arg Leu Pro
245 250 255Met Pro Pro Asn Cys Pro Pro Thr Leu Tyr Ser Leu Met Thr Lys Cys
260 265 270

Trp Ala Tyr Asp Pro Ser Arg Arg Pro Arg Phe Thr Glu Leu Lys Ala
 275 280 285
 Gln Leu Ser Thr Ile Leu Glu Glu Glu Lys Ala Gln Gln Glu Glu Arg
 290 295 300
 Met Arg Met Glu Ser Arg
 305 310

<210> 10
 <211> 273
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: SRC tyrosine kinase
 sequence

<400> 10
 Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly
 1 5 10 15

Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Arg Val
 20 25 30

Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Glu Ala Phe Leu
 35 40 45

Gln Glu Ala Gln Val Met Lys Lys Leu Arg His Glu Lys Leu Val Gln
 50 55 60

Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Tyr
 65 70 75 80

Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Gly Glu Thr Gly Lys
 85 90 95

Tyr Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Ser
 100 105 110

Gly Met Ala Tyr Val Glu Arg Met Asn Tyr Val His Arg Asp Leu Arg
 115 120 125

Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Val Ala Asp
 130 135 140

Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln
 145 150 155 160

Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr
 165 170 175

Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
 180 185 190

Thr Glu Leu Thr Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn
 195 200 205
 Arg Glu Val Leu Asp Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro
 210 215 220
 Pro Glu Cys Pro Glu Ser Leu His Asp Leu Met Cys Gln Cys Trp Arg
 225 230 235 240
 Lys Glu Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ala Phe Leu
 245 250 255
 Glu Asp Tyr Phe Thr Ser Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn
 260 265 270
 Leu

<210> 11

<211> 271

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: HCK tyrosine kinase sequence

<400> 11

Glu Ile Pro Arg Glu Ser Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly
 1 5 10 15

Gln Phe Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val
 20 25 30

Ala Val Lys Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu
 35 40 45

Ala Glu Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys
 50 55 60

Leu His Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe
 65 70 75 80

Met Ala Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser
 85 90 95

Lys Gln Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu
 100 105 110

Gly Met Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg
 115 120 125

Ala Ala Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp
 130 135 140

Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu
 145 150 155 160
 Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe
 165 170 175
 Gly Ser Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
 180 185 190
 Met Glu Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn
 195 200 205
 Pro Glu Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro
 210 215 220
 Glu Asn Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys
 225 230 235 240
 Asn Arg Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu
 245 250 255
 Asp Asp Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Glu Glu Ile Pro
 260 265 270

<210> 12

<211> 263

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: LCK tyrosine kinase
sequence

<400> 12

Glu Val Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly
1 5 10 15

Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val
20 25 30

Ala Val Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu
35 40 45

Ala Glu Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg
50 55 60

Leu Tyr Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr
65 70 75 80

Met Glu Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile
85 90 95

Lys Leu Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu
100 105 110

Gly Met Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg
 115 120 125

Ala Ala Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp
 130 135 140

Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu
 145 150 155 160

Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr
 165 170 175

Gly Thr Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
 180 185 190

Thr Glu Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn
 195 200 205

Pro Glu Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro
 210 215 220

Asp Asn Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys
 225 230 235 240

Glu Arg Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu
 245 250 255

Glu Asp Phe Phe Thr Ala Thr
 260

<210> 13
 <211> 263
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: ABL1 tyrosine kinase
 sequence

<400> 13
 Glu Met Glu Arg Thr Asp Ile Thr Met Lys His Lys Leu Gly Gly Gly
 1 5 10 15

Gln Tyr Gly Glu Val Tyr Glu Gly Val Trp Lys Lys Tyr Ser Leu Thr
 20 25 30

Val Ala Val Lys Thr Leu Lys Glu Asp Thr Met Glu Val Glu Glu Phe
 35 40 45

Leu Lys Glu Ala Ala Val Met Lys Glu Ile Lys His Pro Asn Leu Val
 50 55 60

Gln Leu Leu Gly Val Cys Thr Arg Glu Pro Pro Phe Tyr Ile Ile Thr
 65 70 75 80

<210> 14
<211> 260
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: CSK tyrosine kinase
sequence

<400> 14
Ala Leu Asn Met Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly
1 5 10 15

Glu	Phe	Gly	Asp	Val	Met	Leu	Gly	Asp	Tyr	Arg	Gly	Asn	Lys	Val	Ala	
														20	25	30

Val	Lys	Cys	Ile	Lys	Asn	Asp	Ala	Thr	Ala	Gln	Ala	Phe	Leu	Ala	Glut		
															35	40	45

Ala Ser Val Met Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu
 50 55 60

Gly Val Ile Val Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr
 65 70 75 80

Met Ala Lys Gly Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser
 85 90 95

Val Leu Gly Gly Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu
 100 105 110

Ala Met Glu Tyr Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala
 115 120 125

Ala Arg Asn Val Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp
 130 135 140

Phe Gly Leu Thr Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu
 145 150 155 160

Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser
 165 170 175

Thr Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr
 180 185 190

Ser Phe Gly Arg Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val
 195 200 205

Pro Arg Val Glu Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro
 210 215 220

Pro Ala Val Tyr Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala
 225 230 235 240

Met Arg Pro Ser Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys
 245 250 255

Thr His Glu Leu
 260

<210> 15
 <211> 295
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: TEK tyrosine kinase
 sequence

<400> 15
 Val Leu Asp Trp Asn Asp Ile Lys Phe Gln Asp Val Ile Gly Glu Gly
 1 5 10 15

Asn Phe Gly Gln Val Leu Lys Ala Arg Ile Lys Lys Asp Gly Leu Arg
 20 25 30

Met Asp Ala Ala Ile Lys Arg Met Lys Glu Tyr Ala Ser Lys Asp Asp
 35 40 45

His Arg Asp Phe Ala Gly Glu Leu Glu Val Leu Cys Lys Leu Gly His
 50 55 60

His Pro Asn Ile Ile Asn Leu Leu Gly Ala Cys Glu His Arg Gly Tyr
 65 70 75 80

Leu Tyr Leu Ala Ile Glu Tyr Ala Pro His Gly Asn Leu Leu Asp Phe
 85 90 95

Leu Arg Lys Ser Arg Val Leu Glu Thr Asp Pro Ala Phe Ala Ile Ala
 100 105 110

Asn Ser Thr Ala Ser Thr Leu Ser Ser Gln Gln Leu Leu His Phe Ala
 115 120 125

Ala Asp Val Ala Arg Gly Met Asp Tyr Leu Ser Gln Lys Gln Phe Ile
 130 135 140

His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Gly Glu Asn Tyr Val
 145 150 155 160

Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Gly Gln Glu Val Tyr Val
 165 170 175

Lys Lys Thr Met Gly Arg Leu Pro Val Arg Trp Met Ala Ile Glu Ser
 180 185 190

Leu Asn Tyr Ser Val Tyr Thr Asn Ser Asp Val Trp Ser Tyr Gly
 195 200 205

Val Leu Leu Trp Glu Ile Val Ser Leu Gly Gly Thr Pro Tyr Cys Gly
 210 215 220

Met Thr Cys Ala Glu Leu Tyr Glu Lys Leu Pro Gln Gly Tyr Arg Leu
 225 230 235 240

Glu Lys Pro Leu Asn Cys Asp Asp Glu Val Tyr Asp Leu Met Arg Gln
 245 250 255

Cys Trp Arg Glu Lys Pro Tyr Glu Arg Pro Ser Phe Ala Gln Ile Leu
 260 265 270

Val Ser Leu Asn Arg Met Leu Glu Glu Arg Lys Thr Tyr Val Asn Thr
 275 280 285

Thr Leu Tyr Glu Lys Phe Thr
 290 295

<210> 16
 <211> 291

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: KDR tyrosine kinase
sequence

<400> 16

Glu Phe Pro Arg Asp Arg Leu Lys Leu Gly Lys Pro Leu Gly Arg Gly
1 5 10 15Ala Phe Gly Gln Val Ile Glu Ala Asp Ala Phe Gly Ile Asp Lys Thr
20 25 30Ala Thr Cys Arg Thr Val Ala Val Lys Met Leu Lys Glu Gly Ala Thr
35 40 45His Ser Glu His Arg Ala Leu Met Ser Glu Leu Lys Ile Leu Ile His
50 55 60Ile Gly His His Leu Asn Val Val Asn Leu Leu Gly Ala Cys Thr Lys
65 70 75 80Pro Gly Gly Pro Leu Met Val Ile Val Glu Phe Cys Lys Phe Gly Asn
85 90 95Leu Ser Thr Tyr Leu Arg Ser Lys Arg Asn Glu Phe Val Pro Tyr Lys
100 105 110Val Ala Pro Glu Asp Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu
115 120 125Ile Cys Tyr Ser Phe Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser
130 135 140Arg Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser
145 150 155 160Glu Lys Asn Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile
165 170 175Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro Leu
180 185 190Lys Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr Thr Ile Gln
195 200 205Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Ser Leu
210 215 220Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu Phe Cys Arg
225 230 235 240Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr Thr Thr Pro
245 250 255

Glu Met Tyr Gln Thr Met Leu Asp Cys Trp His Gly Glu Pro Ser Gln
 260 265 270
 Arg Pro Thr Phe Ser Glu Leu Val Glu His Leu Gly Asn Leu Leu Gln
 275 280 285
 Ala Asn Ala
 290

<210> 17
 <211> 290
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: FGFR1 tyrosine kinase sequence

<400> 17
 Glu Leu Pro Arg Asp Arg Leu Val Leu Gly Lys Pro Leu Gly Glu Gly
 1 5 10 15

Ala Phe Gly Gln Val Val Leu Ala Glu Ala Ile Gly Leu Asp Lys Asp
 20 25 30

Lys Pro Asn Arg Val Thr Lys Val Ala Val Lys Met Leu Lys Ser Asp
 35 40 45

Ala Thr Glu Lys Asp Leu Ser Asp Leu Ile Ser Glu Met Glu Met Met
 50 55 60

Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys
 65 70 75 80

Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly
 85 90 95

Asn Leu Arg Glu Tyr Leu Gln Ala Arg Arg Pro Pro Gly Leu Glu Tyr
 100 105 110

Ser Tyr Asn Pro Ser His Asn Pro Glu Glu Gln Leu Ser Ser Lys Asp
 115 120 125

Leu Val Ser Cys Ala Tyr Gln Val Ala Arg Gly Met Glu Tyr Leu Ala
 130 135 140

Ser Lys Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu Val
 145 150 155 160

Thr Glu Asp Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp
 165 170 175

Ile His His Ile Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro
 180 185 190

Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Ile Tyr Thr His
 195 200 205

Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Thr
 210 215 220

Leu Gly Gly Ser Pro Tyr Pro Gly Val Pro Val Glu Glu Leu Phe Lys
 225 230 235 240

Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ser Asn Cys Thr Asn
 245 250 255

Glu Leu Tyr Met Met Arg Asp Cys Trp His Ala Val Pro Ser Gln
 260 265 270

Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Ile Val Ala
 275 280 285

Leu Thr
 290

<210> 18

<211> 294

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: INSR tyrosine kinase
 sequence

<400> 18

Glu Val Ser Arg Glu Lys Ile Thr Leu Leu Arg Glu Leu Gly Gln Gly
 1 5 10 15

Ser Phe Gly Met Val Tyr Glu Gly Asn Ala Arg Asp Ile Ile Lys Gly
 20 25 30

Glu Ala Glu Thr Arg Val Ala Val Lys Thr Val Asn Glu Ser Ala Ser
 35 40 45

Leu Arg Glu Arg Ile Glu Phe Leu Asn Glu Ala Ser Val Met Lys Gly
 50 55 60

Phe Thr Cys His His Val Val Arg Leu Leu Gly Val Val Ser Lys Gly
 65 70 75 80

Gln Pro Thr Leu Val Val Met Glu Leu Met Ala His Gly Asp Leu Lys
 85 90 95

Ser Tyr Leu Arg Ser Leu Arg Pro Glu Ala Glu Asn Asn Pro Gly Arg
 100 105 110

Pro Pro Pro Thr Leu Gln Glu Met Ile Gln Met Ala Ala Glu Ile Ala
 115 120 125

Asp Gly Met Ala Tyr Leu Asn Ala Lys Lys Phe Val His Arg Asp Leu
 130 135 140
 Ala Ala Arg Asn Cys Met Val Ala His Asp Phe Thr Val Lys Ile Gly
 145 150 155 160
 Asp Phe Gly Met Thr Arg Asp Ile Tyr Glu Thr Asp Tyr Tyr Arg Lys
 165 170 175
 Gly Gly Lys Gly Leu Leu Pro Val Arg Trp Met Ala Pro Glu Ser Leu
 180 185 190
 Lys Asp Gly Val Phe Thr Thr Ser Ser Asp Met Trp Ser Phe Gly Val
 195 200 205
 Val Leu Trp Glu Ile Thr Ser Leu Ala Glu Gln Pro Tyr Gln Gly Leu
 210 215 220
 Ser Asn Glu Gln Val Leu Lys Phe Val Met Asp Gly Gly Tyr Leu Asp
 225 230 235 240
 Gln Pro Asp Asn Cys Pro Glu Arg Val Thr Asp Leu Met Arg Met Cys
 245 250 255
 Trp Gln Phe Asn Pro Lys Met Arg Pro Thr Phe Leu Glu Ile Val Asn
 260 265 270
 Leu Leu Lys Asp Asp Leu His Pro Ser Phe Pro Glu Val Ser Phe Phe
 275 280 285
 His Ser Glu Glu Asn Lys
 290

<210> 19
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 19
 Glu Val Ala Arg Glu Lys Ile Thr Met Ser Arg Glu Leu Gly Gln Gly
 1 5 10 15
 Ser Phe Gly Met Val Tyr Glu Gly Val Ala Lys Gly Val Val Lys Asp
 20 25 30
 Glu Pro Glu Thr Arg Val Ala Ile Lys Thr Val Asn Glu Ala Ala Ser
 35 40 45
 Met Arg Glu Arg Ile Glu Phe Leu Asn Glu Ala Ser Val Met Lys Glu
 50 55 60
 Phe Asn Cys His His Val Val Arg Leu Leu Gly Val Val Ser Gln Gly
 65 70 75 80
 Gln Pro Thr Leu Val Ile Met Glu Leu Met Thr Arg Gly Asp Leu Lys
 85 90 95

Ser Tyr Leu Arg Ser Leu Arg Pro Glu Met Glu Asn Asn Pro Val Leu
 100 105 110
 Ala Pro Pro Ser Leu Ser Lys Met Ile Gln Met Ala Gly Glu Ile Ala
 115 120 125
 Asp Gly Met Ala Tyr Leu Asn Ala Asn Lys Phe Val His Arg Asp Leu
 130 135 140
 Ala Ala Arg Asn Cys Met Val Ala Glu Asp Phe Thr Val Lys Ile Gly
 145 150 155 160
 Asp Phe Gly Met Thr Arg Asp Ile Tyr Glu Thr Asp Tyr Tyr Arg Lys
 165 170 175
 Gly Gly Lys Gly Leu Leu Pro Val Arg Trp Met Ser Pro Glu Ser Leu
 180 185 190
 Lys Asp Gly Val Phe Thr Thr Tyr Ser Asp Val Trp Ser Phe Gly Val
 195 200 205
 Val Leu Trp Glu Ile Ala Thr Leu Ala Glu Gln Pro Tyr Gln Gly Leu
 210 215 220
 Ser Asn Glu Gln Val Leu Arg Phe Val Met Glu Gly Gly Leu Leu Asp
 225 230 235 240
 Lys Pro Asp Asn Cys Pro Asp Met Leu Leu Glu Leu Met Arg Met Cys
 245 250 255
 Trp Gln Tyr Asn Pro Lys Met Arg Pro Ser Phe Leu Glu Ile Ile Ser
 260 265 270
 Ser Ile Lys Glu Glu Met Glu Pro Gly Phe Arg Glu Val Ser Phe Tyr
 275 280 285
 Tyr Ser Glu Glu Asn Lys
 290

<210> 20
 <211> 278
 <212> PRT
 <213> Unknown Organism

 <220>
 <223> Description of Unknown Organism: EPHB2 tyrosine kinase
 sequence

 <400> 20
 Glu Ile Asp Ile Ser Cys Val Lys Ile Glu Gln Val Ile Gly Ala Gly
 1 5 10 15

 Glu Phe Gly Glu Val Cys Ser Gly His Leu Lys Leu Pro Gly Lys Arg
 20 25 30

Glu Ile Phe Val Ala Ile Lys Thr Leu Lys Ser Gly Tyr Thr Glu Lys
 35 40 45

Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met Gly Gln Phe Asp
 50 55 60

His Pro Asn Val Ile His Leu Glu Gly Val Val Thr Lys Ser Thr Pro
 65 70 75 80

Val Met Ile Ile Thr Glu Phe Met Glu Asn Gly Ser Leu Asp Ser Phe
 85 90 95

Leu Arg Gln Asn Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met
 100 105 110

Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asp Met Asn Tyr
 115 120 125

Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu
 130 135 140

Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Phe Leu Glu Asp Asp
 145 150 155 160

Thr Ser Asp Pro Thr Tyr Thr Ser Ala Leu Gly Gly Lys Ile Pro Ile
 165 170 175

Arg Trp Thr Ala Pro Glu Ala Ile Gln Tyr Arg Lys Phe Thr Ser Ala
 180 185 190

Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr
 195 200 205

Gly Glu Arg Pro Tyr Trp Asp Met Thr Asn Gln Asp Val Ile Asn Ala
 210 215 220

Ile Glu Gln Asp Tyr Arg Leu Pro Pro Met Asp Cys Pro Ser Ala
 225 230 235 240

Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Asp Arg Asn His Arg
 245 250 255

Pro Lys Phe Gly Gln Ile Val Asn Thr Leu Asp Lys Met Ile Arg Asn
 260 265 270

Pro Asn Ser Leu Lys Ala
 275

<210> 21

<211> 283

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: EGFR tyrosine kinase sequence

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 Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu Lys
 20 25 30
 Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser Pro
 35 40 45
 Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser Val
 50 55 60
 Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr
 65 70 75 80
 Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp Tyr
 85 90 95
 Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn Trp
 100 105 110
 Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg Leu
 115 120 125
 Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro Gln
 130 135 140
 His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala Glu
 145 150 155 160
 Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp Met
 165 170 175
 Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp Val
 180 185 190
 Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser Lys
 195 200 205
 Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu Lys
 210 215 220
 Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met
 225 230 235 240
 Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys Phe
 245 250 255
 Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln Arg
 260 265 270
 Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His
 275 280

<210> 22
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 6-His tag

<400> 22
His His His His His His
1 5

<210> 23
<211> 8
<212> PRT
<213> Homo sapiens

<400> 23
Asp Ile Tyr Ala Glu Ile Pro Asp
1 5

<210> 24
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
pET15S peptide fragment

<400> 24
Gly Ser His Met
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<210> 25
<211> 7
<212> PRT
<213> Homo sapiens

<400> 25
Ile Tyr Ala Glu Ile Pro Asp
1 5